

Sample: SRR1239339

FASTQ Quality

Filename	SRR1239339_R1.fastq.gz	SRR1239339_R2.fastq.gz
File Size	171.3 MB	184.9 MB
Q30 Passing	72.45%	59.6%
Mean Read Score	12.5	7.3
Average Read Length	301	301

Read Mapping against SRR1239339

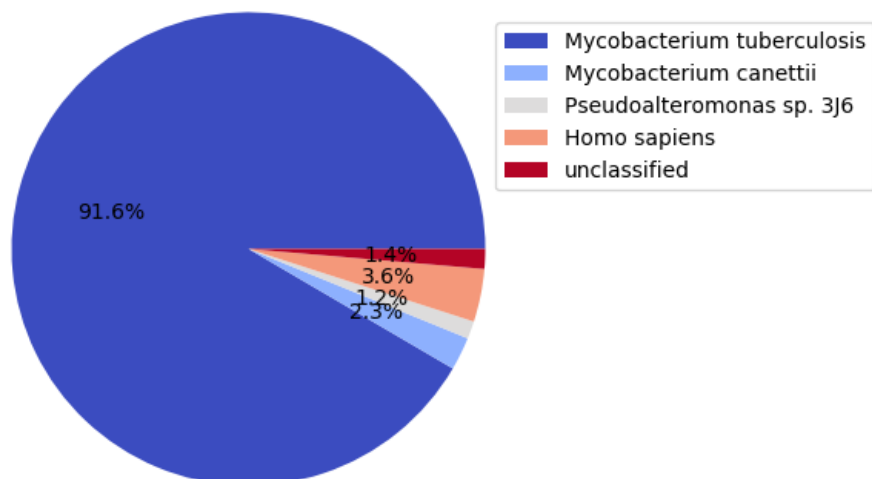
Mapped Paired Reads	Mapped Single Reads	Unmapped Reads	Unmapped Percent	Unmapped Assembled Contigs	
1,084,031	8,124	21,938	2.0%	assembly not done	
Duplicate Paired Reads	Duplicate Single Reads	Duplicate Percent of Mapped Reads			
60,274	3,914	5.7%			
BAM File	Reference Length	Genome with Coverage	Average Depth	No Coverage Bases	Quality SNPs
SRR1239339_nodup.bam	5,059,216	99.94%	75.0X	3,026	913

Assembly

Contig count	Contig length counts < 301-999bp >	Longest contig	Total length	N50	FASTQ calculated mean coverage
1,508	44 1,286 178	160,760	5,059,216	57,538	130.8X

FASTQ Identifications

FASTQ Read Identification



Identified using: Kraken and Bracken

Genome Size Comparisons

Mycobacterium tuberculosis	expected: 4,075,000 nt
SRR1239339	assembled: 5,059,216 nt

Sourmash Sequence Similarity

Similarity	ID
86.4%	KK338833.1 Mycobacterium africanum MAL010071 genomic scaffold adPeu-supercont1.1, whole genome shotgun sequence
86.4%	CPWI01000001.1 Mycobacterium tuberculosis genome assembly 8080_831, scaffold ERS124377SCcontig000001, whole genome shotgun sequence
86.4%	KK357085.1 Mycobacterium tuberculosis BTB11-207 genomic scaffold adTze-supercont1.1, whole genome shotgun sequence
86.4%	KK339435.1 Mycobacterium tuberculosis OFXR-22 genomic scaffold adiej-supercont1.1, whole genome shotgun sequence
86.4%	KK338951.1 Mycobacterium africanum MAL010129 genomic scaffold adPiQ-supercont1.1, whole genome shotgun sequence
86.4%	CPWC01000001.1 Mycobacterium tuberculosis genome assembly 8080_832, scaffold ERS124378SCcontig000001, whole genome shotgun sequence
86.4%	KK328887.1 Mycobacterium tuberculosis M1448 genomic scaffold adOZd-supercont1.1, whole genome shotgun sequence
86.4%	KK339113.1 Mycobacterium africanum MAL020135 genomic scaffold adPaG-supercont1.1, whole genome shotgun sequence
86.4%	KK338880.1 Mycobacterium africanum MAL010100 genomic scaffold adPak-supercont1.1, whole genome shotgun sequence
86.4%	KK328761.1 Mycobacterium tuberculosis M1424 genomic scaffold adPcq-supercont1.1, whole genome shotgun sequence

MLST 2.19.0

Schema-Sequence type: **mycobacteria-215**

MLST Detail: S14Z(17), L35(15), S19(20), L19(19), S12(20), S8(18), L16(22), S7(19)

Results provided by: MLST

AMRFinderPlus - version 3.11.2, database 2021-03-01.1

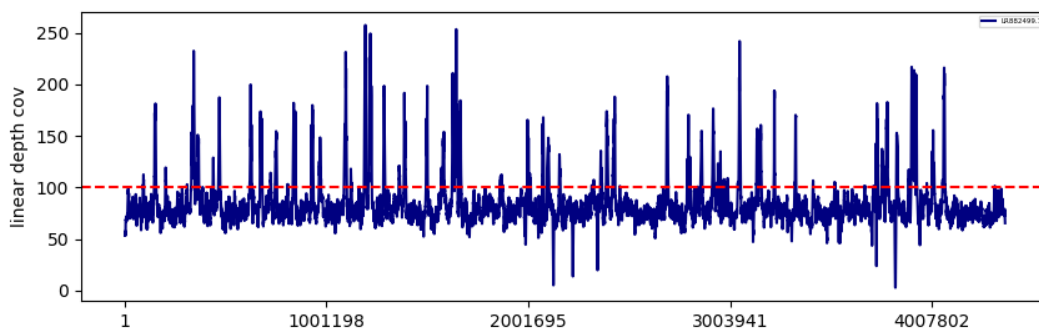
AMRFinderPlus Organism Option Not Found: Mycobacterium tuberculosis

Contig ID	Element	Gene	Description	% Cov	% Similar
NODE_43_length_39370_cov_24.371659	AMR	erm(37)	23S rRNA (adenine(2058)-N(6))-methyltransferase Erm(37)	100.0%	100.0%
NODE_56_length_29591_cov_28.830301	AMR	blaC	class A beta-lactamase BlaC	100.0%	100.0%
NODE_62_length_26894_cov_29.245900	AMR	aac(2')-Ic	aminoglycoside N-acetyltransferase AAC(2')-Ic	100.0%	100.0%

Results provided by: AMRFinderPlus

Coverage Graph

SRR1239339 reads aligned against LR882499



ID	Average Depth	Genome Coverage	Genome Length	Ambiguous SNPs
LR882499.1	84.8X	99.8%	4,369,915	300

ID Detail

LR882499.1 Mycobacterium tuberculosis variant microti OV254 strain Mycobacterium microti OV254 genom

BLAST nt - Assembly Identification

Nucleotide Representa- tion	Description
781,799	LR882499 Mycobacterium tuberculosis variant microti OV254 strain Mycobacterium microti OV254 genome
762,477	LR882500 Mycobacterium tuberculosis variant microti strain Mycobacterium microti 94-2272 genome asse
742,413	LR882496 Mycobacterium tuberculosis variant microti strain Mycobacterium microti ATCC 35782 genome a
436,732	LR882498 Mycobacterium tuberculosis variant microti strain Mycobacterium microti Maus III genome ass
323,054	CP010333 Mycobacterium tuberculosis variant microti strain 12 chromosome, complete genome
160,760	CP096840 Mycobacterium tuberculosis variant bovis strain Mb2269 chromosome, complete genome
137,145	CP007803 Mycobacterium tuberculosis K, complete genome
131,350	CP014617 Mycobacterium africanum strain UT307 genome
104,454	CP016401 Mycobacterium caprae strain Allgaeu genome
96,583	CP010337 Mycobacterium tuberculosis strain 22115 chromosome, complete genome
85,364	CP069068 Mycobacterium tuberculosis strain N1272 chromosome, complete genome
84,358	LR882497 Mycobacterium tuberculosis variant microti strain Mycobacterium microti Maus IV genome asse
69,629	CP010336 Mycobacterium tuberculosis strain 2279 chromosome, complete genome
62,831	CP117298 Mycobacterium tuberculosis variant bovis strain OLF-AH-2022-TB-0122 chromosome, complete ge
59,469	CP023629 Mycobacterium tuberculosis strain MDRMA2260 chromosome, complete genome
53,025	CP043639 Sphingomonas sp. NBWT7 chromosome, complete genome
39,947	CP089772 Mycobacterium tuberculosis strain I0003165-3 chromosome, complete genome
39,920	CP095022 Mycobacterium tuberculosis strain SGF0472017 chromosome, complete genome
37,719	CP069076 Mycobacterium tuberculosis strain N0031 chromosome, complete genome
35,212	CP054014 Mycobacterium tuberculosis strain FDAARGOS_756 chromosome, complete genome
33,608	CP086594 Sphingomonas radiodurans strain S9-5 chromosome, complete genome
26,894	CP096843 Mycobacterium tuberculosis variant bovis strain Mb3602 chromosome, complete genome
24,970	CP118289 Streptococcus pneumoniae D39 chromosome
23,269	CP047163 Mycobacterium tuberculosis strain TCDC7 chromosome
17,642	CP054013 Mycobacterium tuberculosis strain FDAARGOS_757 chromosome, complete genome
17,506	CP047258 Mycobacterium tuberculosis strain TCDC3 chromosome
16,970	CP046308 Mycobacterium tuberculosis strain FDAARGOS_751 chromosome, complete genome
11,683	CP050137 Sphingomonas sp. CL5.1 chromosome, complete genome
11,171	LR699570 Mycobacterium tuberculosis variant bovis strain Mb3601 genome assembly, chromosome: Mb3601
11,092	CP034516 Eukaryotic synthetic construct chromosome 13
10,262	CP069067 Mycobacterium tuberculosis strain N1268 chromosome, complete genome
10,122	MK327937 Escherichia phage vB_EcoM_G10400, complete genome
8,948	CP048071 Mycobacterium tuberculosis strain RW-TB008 chromosome, complete genome
8,439	CP034492 Eukaryotic synthetic construct chromosome 14
7,758	CP045962 Mycobacterium tuberculosis strain AUSMDU00018547 chromosome, complete genome
7,211	CP034496 Eukaryotic synthetic construct chromosome 18
7,090	CP034493 Eukaryotic synthetic construct chromosome 15
6,781	CP034499 Eukaryotic synthetic construct chromosome 20
6,693	CP034495 Eukaryotic synthetic construct chromosome 17
6,282	CP017578 Sphingomonas melonis TY, complete genome
6,186	CP068256 Homo sapiens isolate CHM13 chromosome 22
5,964	CP053022 Sphingobium yanoikuyae strain YC-XJ2 plasmid p-A-Sy, complete sequence
5,896	CP096971 Sphingomonas sp. SUN019 chromosome, complete genome
5,215	CP018301 Mycobacterium tuberculosis strain I0002801-4, complete genome
5,182	CP115900 Sphingomonas sp. CV7422 chromosome, complete genome
5,144	CP029985 Sphingomonas sp. FARSPH chromosome, complete genome
5,127	CP025604 Mycobacterium tuberculosis strain GG-129-11 chromosome, complete genome
5,066	CP053092 Mycobacterium tuberculosis strain 4860 chromosome, complete genome
5,002	CP034494 Eukaryotic synthetic construct chromosome 16
4,575	CP061036 Sphingomonas aliaeris strain DH-S5 plasmid punnamed1, complete sequence
4,508	CP027035 Mycobacterium tuberculosis variant bovis strain 2002/0476 chromosome, complete genome
4,419	OX419548 Homo sapiens genome assembly, chromosome: Y
4,249	CP068263 Homo sapiens isolate CHM13 chromosome 15
3,585	CP040832 Mycobacterium tuberculosis variant bovis strain 1 chromosome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
3,479	CP048422 <i>Sphingomonas insulae</i> strain KCTC 12872 chromosome, complete genome
3,425	OX419651 <i>Homo sapiens</i> genome assembly, chromosome: Y
3,375	OW052570 <i>Mycobacterium tuberculosis</i> strain Lineage 1.1.2 genome assembly, chromosome: 1
3,318	LN899827 <i>Ralstonia solanacearum</i> genome assembly 9 genomes, chromosome : IX
3,315	CP068258 <i>Homo sapiens</i> isolate CHM13 chromosome 20
3,281	OX419549 <i>Homo sapiens</i> genome assembly, chromosome: Y
3,161	LN899822 <i>Ralstonia solanacearum</i> genome assembly 9 genomes, chromosome : IV
3,086	CP034500 Eukaryotic synthetic construct chromosome 21
3,056	CP009431 <i>Sphingopyxis macrogoltabida</i> strain 203 plasmid unnamed, complete sequence
2,923	CP034522 Eukaryotic synthetic construct chromosome 19
2,915	CP068262 <i>Homo sapiens</i> isolate CHM13 chromosome 16
2,880	CP117412 <i>Sphingomonas naphthae</i> strain KACC 18716 plasmid unnamed1, complete sequence
2,865	CP041803 <i>Mycobacterium tuberculosis</i> strain SEA11278P6C4 chromosome, complete genome
2,787	CP023705 <i>Sphingomonas melonis</i> strain ZJ26 chromosome, complete genome
2,709	CP090059 <i>Sphingomonas cannabina</i> strain DM2-R-LB4 chromosome, complete genome
2,560	CP013916 <i>Sphingomonas</i> sp. LK11, complete genome
2,504	AP022673 <i>Sphingomonas</i> sp. HMP9 DNA, complete genome
2,492	CP068257 <i>Homo sapiens</i> isolate CHM13 chromosome 21
2,451	CP034501 Eukaryotic synthetic construct chromosome 22
2,350	LN899820 <i>Ralstonia solanacearum</i> genome assembly 9 genomes, chromosome : II
2,209	CP119315 MAG: <i>Sphingomonas</i> sp. isolate MAG 27 chromosome, complete genome
2,197	CP117026 <i>Sphingomonas hankookensis</i> strain SZ.B2R2 plasmid pSZ.B2R2_1, complete sequence
2,145	CP099619 <i>Sphingomonadaceae</i> bacterium OTU29MARTA1 chromosome, complete genome
1,939	CP068261 <i>Homo sapiens</i> isolate CHM13 chromosome 17
1,938	CP085578 <i>Mycobacterium tuberculosis</i> strain 25/2016 chromosome
1,901	CP115174 <i>Sphingomonas</i> sp. PAMB00755 chromosome, complete genome
1,837	CP015583 <i>Roseomonas gilardii</i> strain U14-5 chromosome 1, complete sequence
1,786	CP098762 <i>Sphingomonas aerolata</i> strain PDD-32b-11 chromosome, complete genome
1,719	CP088296 <i>Sphingomonas</i> sp. J315 chromosome
1,708	CP117025 <i>Sphingomonas hankookensis</i> strain SZ.B2R2 chromosome, complete genome
1,657	LN899821 <i>Ralstonia solanacearum</i> genome assembly 9 genomes, chromosome : III
1,636	CP035765 <i>Sphingomonas paucimobilis</i> strain AIMST S2 chromosome, complete genome
1,616	CP053226 <i>Sphingobium</i> sp. RSMS plasmid pRSMS3, complete sequence
1,449	CP005083 <i>Sphingobium</i> sp. TKS chromosome 1, complete sequence
1,443	CP019511 <i>Sphingomonas</i> sp. LM7, complete genome
1,435	AP023850 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0365
1,414	NG_051298 <i>Homo sapiens</i> sidekick cell adhesion molecule 1 (SDK1), RefSeqGene on chromosome 7
1,412	AL603755 Human DNA sequence from clone RP11-136G2 on chromosome 6, complete sequence
1,397	CP010836 <i>Sphingomonas hengshuiensis</i> strain WHSC-8, complete genome
1,394	CP090953 <i>Sphingomonas</i> sp. S2-65 chromosome, complete genome
1,383	CP039249 <i>Sphingomonas</i> sp. PAMC26645 chromosome, complete genome
1,359	CP014168 <i>Sphingomonas panacis</i> strain DCY99, complete genome
1,242	AP023845 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0360
1,216	CP009571 <i>Sphingomonas taxi</i> strain ATCC 55669, complete genome
1,201	LS997768 <i>Homo sapiens</i> genome assembly, organelle: mitochondrion
1,187	CP023581 <i>Mycobacterium tuberculosis</i> strain LN2358 chromosome, complete genome
1,175	CP069074 <i>Mycobacterium tuberculosis</i> strain N1274 chromosome, complete genome
1,175	CP018820 <i>Sphingomonas koreensis</i> strain ABOJV chromosome, complete genome
1,172	CP060782 <i>Sphingomonas sediminicola</i> strain KACC 15039 chromosome, complete genome
1,171	CP096040 <i>Caulobacter segnis</i> strain RL271 chromosome, complete genome
1,155	CP015521 <i>Sphingomonas</i> sp. NIC1, complete genome
1,149	AP024036 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0551
1,144	M64779 Human D8Z2 gene, partial sequence
1,133	AP023669 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0184

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
1,078	LN899826 <i>Ralstonia solanacearum</i> genome assembly 9 genomes, chromosome : VIII
1,069	LR588407 <i>Brevundimonas vancouveriensis</i> strain NCTC9239 genome assembly, chromosome: 1
1,054	CP046254 <i>Sphingobium</i> sp. CAP-1 plasmid p1, complete sequence
1,049	CP023741 <i>Sphingobium yanoikuyae</i> strain S72 chromosome, complete genome
1,029	CP117411 <i>Sphingomonas naphthae</i> strain KACC 18716 chromosome, complete genome
1,021	CP046309 <i>Mycobacterium tuberculosis</i> strain FDAARGOS_750 chromosome, complete genome
1,015	CP053346 <i>Sphingomonas</i> sp. AP4-R1 chromosome, complete genome
1,008	CP099621 <i>Sphingomonadaceae</i> bacterium OTU29THOMA1 chromosome, complete genome
1,001	AP023480 <i>Homo sapiens</i> DNA, chromosome 20, nearly complete genome
989	AP023478 <i>Homo sapiens</i> DNA, chromosome 18, nearly complete genome
977	AP023708 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0223
961	CP074376 <i>Mycobacterium neoaurum</i> strain MN2019 chromosome, complete genome
960	AP002026 <i>Homo sapiens</i> genomic DNA, chromosome 4q22-q24, clone:429K21, complete sequence
955	AP017661 <i>Sphingobium cloacae</i> plasmid pSCLO_7 DNA, complete sequence, strain: JCM 10874
953	MN849868 <i>Homo sapiens</i> isolate PNG99 haplogroup Q1a mitochondrion, complete genome
930	NG_051047 <i>Homo sapiens</i> unc-51 like kinase 4 (ULK4), RefSeqGene on chromosome 3
926	AP022672 <i>Sphingomonas</i> sp. HMP6 DNA, complete genome
911	CP061080 <i>Aquibium microcystis</i> strain NIBR3 chromosome, complete genome
906	AL356986 Human DNA sequence from clone RP11-395N6 on chromosome 1, complete sequence
901	CP043498 <i>Rhizobium grahamii</i> strain BG7 chromosome, complete genome
898	AP023784 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0299
897	CP034497 Eukaryotic synthetic construct chromosome 19
894	CP041016 <i>Sphingobium fuliginis</i> ATCC 27551 chromosome cSF1, complete sequence
872	CP009572 <i>Sphingomonas taxi</i> strain ATCC 55669 plasmid STP1, complete sequence
872	AC073149 <i>Homo sapiens</i> BAC clone RP11-803F15 from 2, complete sequence
807	AP024059 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0574
806	AP023981 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0496
789	AC099050 <i>Homo sapiens</i> chromosome 3 clone RP11-413B21, complete sequence
761	AP023626 <i>Homo sapiens</i> DNA, sequence_id: unplaced_0141
753	CP011310 <i>Aurantibacter atlanticus</i> strain s21-N3 chromosome, complete genome
739	AC104838 <i>Homo sapiens</i> chromosome 1 clone RP4-671I22, complete sequence
730	CP069065 <i>Mycobacterium tuberculosis</i> strain N0091 chromosome, complete genome
724	CP010957 <i>Sphingobium</i> sp. YBL2 plasmid 3pYBL2-3, complete sequence
715	MN559812 <i>Sphingomonas olei</i> strain 19SCL-58 16S ribosomal RNA gene, partial sequence
706	CP023452 <i>Rhizorhabdus dicambivorans</i> strain Ndbn-20 plasmid p3, complete sequence
700	CP018221 <i>Tardibacter chloracetimidivorans</i> strain JJ-A5 chromosome, complete genome
697	LN899823 <i>Ralstonia solanacearum</i> genome assembly 9 genomes, chromosome : V
696	CP046535 <i>Sphingomonas profundus</i> strain LMO-1 chromosome, complete genome
693	NG_029445 <i>Homo sapiens</i> proprotein convertase subtilisin/kexin type 5 (PCSK5), RefSeqGene on chromos
689	LT840185 <i>Sphingomonas indica</i> strain Dd16 genome assembly, chromosome: I
687	NM_001047434 <i>Homo sapiens</i> diphthamide biosynthesis 3 (DPH3), transcript variant 2, mRNA
665	CP012669 <i>Altererythrobacter epoxidivorans</i> strain CGMCC 1.7731 chromosome, complete genome
656	ON249121 <i>Homo sapiens</i> SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1) gene, complete cds
651	CP007514 <i>Rubrobacter radiotolerans</i> strain RSPS-4, complete genome
649	CP110111 <i>Sphingomonas</i> sp. R1 chromosome, complete genome
648	AC117395 <i>Homo sapiens</i> 3 BAC RP11-651P23 (Roswell Park Cancer Institute Human BAC Library) complete s
647	CP034179 <i>Caenibius tardaugens</i> NBRC 16725 chromosome, complete genome
636	MK860678 <i>Homo sapiens</i> isolate WANA062 haplogroup B2 mitochondrion, complete genome
635	CP002013 <i>Burkholderia</i> sp. CCGE1002 chromosome 1, complete sequence
631	CP044117 <i>Roseomonas mucosa</i> strain FDAARGOS_658 chromosome 4, complete sequence
631	CP091804 <i>Sphingopyxis</i> sp. BSN-002 chromosome
631	AC069543 <i>Homo sapiens</i> chromosome 10 clone RP11-393H5, complete sequence
629	CP004036 <i>Sphingomonas</i> sp. MM-1, complete genome
625	CP030941 <i>Nitratireductor thuwali</i> strain Nit1536 chromosome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
618	AC073912 Homo sapiens 12 BAC RP11-989F5 (Roswell Park Cancer Institute Human BAC Library) complete s
617	CP009293 Novosphingobium pentaromativorans US6-1 plasmid pLA4, complete sequence
617	NG_008213 Homo sapiens transmembrane channel like 1 (TMC1), RefSeqGene on chromosome 9
612	AP000843 Homo sapiens genomic DNA, chromosome 11 clone:RP11-684N3, complete sequence
608	AP023800 Homo sapiens DNA, sequence_id: unplaced_0315
608	AC278971 Homo sapiens chromosome 15 clone VMRC59-26B10, complete sequence
607	AC092035 Homo sapiens chromosome 3 clone RP11-72H11, complete sequence
603	AC005046 Homo sapiens BAC clone CTB-13F3 from 7q22, complete sequence
600	CP110113 Sphingomonas sp. R1 plasmid pR1b, complete sequence
599	LT708304 Mycobacterium bovis AF2122/97 genome assembly, chromosome: Mycobacterium_bovis_AF212297
597	CP130814 Mycobacterium tuberculosis strain MTb-Oman-321528 chromosome, complete genome
597	FR687359 Burkholderia rhizoxinica HKI 454, complete genome
596	CP086569 Homo sapiens isolate NA24385 chromosome Y
593	NG_028228 Homo sapiens ADAM metalloproteinase with thrombospondin type 1 motif 20 (ADAMTS20), RefSeq
590	AL035425 Human DNA sequence from clone RP6-24A23 on chromosome Xq22.2-23, complete sequence
587	AC007394 Homo sapiens BAC clone RP11-489G12 from 2, complete sequence
587	CP013389 Burkholderia mayonis strain BDU8 chromosome 1, complete sequence
578	CP019612 Mycobacterium tuberculosis strain H107 chromosome, complete genome
577	AC130304 Homo sapiens chromosome 8, clone RP11-205M5, complete sequence
575	NG_053027 Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), RefSeqGene on chromosome
575	CP113097 Pseudomonas putida strain WYTS.T61 chromosome, complete genome
573	CP059322 Micromonospora ferruginea strain 28ISP2-46 chromosome, complete genome
569	KY962518 Homo sapiens external transcribed spacer 18S ribosomal RNA gene, internal transcribed space
563	AC279516 Homo sapiens chromosome unknown clone VMRC59-396P01, complete sequence
562	CP096972 Sphingomonas sp. SUN039 chromosome, complete genome
562	AL358787 Human DNA sequence from clone RP11-181F12 on chromosome 10, complete sequence
561	HG938353 Neorhizobium galegae, complete genome
560	CP035501 Sphingosinella sp. BN140058 chromosome, complete genome
554	CP041853 Mycobacterium tuberculosis strain 1-0107P6C4 chromosome, complete genome
553	AL353766 Human DNA sequence from clone RP11-400A24 on chromosome 9, complete sequence
552	AL390242 Human DNA sequence from clone RP11-31F15 on chromosome 1p13.1-13.3, complete sequence
549	CP047218 Sphingobium yanoikuyae strain YC-JY1 chromosome, complete genome
549	AC012669 Homo sapiens BAC clone RP11-512G4 from 2, complete sequence
548	NG_032009 Homo sapiens WAS/WASL interacting protein family member 1 (WIPF1), RefSeqGene (LRG_374)
548	AC278857 Homo sapiens chromosome 10 clone VMRC59-053C06, complete sequence
547	AL390961 Human DNA sequence from clone RP13-16H11 on chromosome 10, complete sequence
543	AP018664 Sphingobium amniense DSM 16289 DNA, complete genome
542	AP023706 Homo sapiens DNA, sequence_id: unplaced_0221
541	AC117383 Homo sapiens 3 BAC RP11-789L4 (Roswell Park Cancer Institute Human BAC Library) complete se
541	AC091854 Homo sapiens chromosome 5 clone CTD-2293C22, complete sequence
541	AC112242 Homo sapiens BAC clone RP11-503L23 from 4, complete sequence
540	AL365199 Human DNA sequence from clone RP11-124O11 on chromosome 10, complete sequence
539	BK000438 TPA_exp: Homo sapiens RING finger protein COP1 gene, complete cds
539	AC093669 Homo sapiens BAC clone RP11-540E16 from 4, complete sequence
538	CP040883 Staphylococcus epidermidis strain O47 chromosome, complete genome
537	CP039349 Vigna unguiculata cultivar Xiabao 2 chromosome Vu04
537	AC008376 Homo sapiens chromosome 5 clone CTC-207P7, complete sequence
536	AL590368 Human DNA sequence from clone RP11-3K19 on chromosome 9, complete sequence
535	AC016651 Homo sapiens chromosome 5 clone RP1-251I12, complete sequence
534	AC017104 Homo sapiens BAC clone RP11-562I5 from 2, complete sequence
533	AC008243 Homo sapiens, clone RP11-45L9, complete sequence
532	CP025061 Roseomonas mucosa strain PG chromosome, complete genome
530	AL589825 Human DNA sequence from clone RP11-12K1 on chromosome 9, complete sequence
530	NG_033878 Homo sapiens dipeptidyl peptidase like 6 (DPP6), RefSeqGene on chromosome 7

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
528	CP061035 <i>Sphingomonas aliaeris</i> strain DH-S5 chromosome, complete genome
528	AL390835 Human DNA sequence from clone RP5-1119O21 on chromosome 10, complete sequence
526	AC016637 Homo sapiens chromosome 5 clone RP11-34J15, complete sequence
526	AC068457 Homo sapiens chromosome 11, clone RP11-582N4, complete sequence
526	AC026723 Homo sapiens chromosome 5 clone CTD-2209N14, complete sequence
526	AC079237 Homo sapiens BAC clone RP11-711J3 from 4, complete sequence
526	AL356357 Human DNA sequence from clone RP4-550F15 on chromosome 1, complete sequence
525	NG_012877 Homo sapiens protoporphyrinogen oxidase (PPOX), RefSeqGene (LRG_1078) on chromosome 1
525	AC099568 Homo sapiens chromosome 1 clone RP5-943J3, complete sequence
524	AL671985 Human DNA sequence from clone RP11-463N8 on chromosome 1, complete sequence
523	CP089927 <i>Mycobacterium tuberculosis</i> strain M20 chromosome, complete genome
522	NG_011445 Homo sapiens FER tyrosine kinase (FER), RefSeqGene on chromosome 5
521	AL445186 Human DNA sequence from clone RP11-336P12 on chromosome 9, complete sequence
520	AC278991 Homo sapiens chromosome 15 clone VMRC59-359A02, complete sequence
519	AC093860 Homo sapiens BAC clone RP11-538D9 from 4, complete sequence
519	AL672045 Human DNA sequence from clone RP11-577O19 on chromosome 1, complete sequence
519	NG_008255 Homo sapiens solute carrier family 19 member 2 (SLC19A2), RefSeqGene on chromosome 1
519	AC122710 Homo sapiens chromosome 5 clone RP11-332J15, complete sequence
519	AC112723 Homo sapiens BAC clone RP11-785D16 from 2, complete sequence
518	NG_029728 Homo sapiens protein kinase cAMP-activated catalytic subunit beta (PRKACB), RefSeqGene on
518	AC055723 Homo sapiens 3 BAC RP11-201E8 (Roswell Park Cancer Institute Human BAC Library) complete se
517	KF163015 Homo sapiens isolate 97381 mitochondrion, complete genome
517	AC079631 Homo sapiens 12 BAC RP11-389G16 (Roswell Park Cancer Institute Human BAC Library) complete
517	AL359644 Human DNA sequence from clone RP11-162D16 on chromosome 9, complete sequence
516	AL391829 Human DNA sequence from clone RP11-124B11 on chromosome 6, complete sequence
516	CP012646 <i>Streptococcus mitis</i> strain KCOM 1350 (= ChDC B183), complete genome
516	AC092468 Homo sapiens 3 BAC RP11-326J18 (Roswell Park Cancer Institute Human BAC Library) complete s
516	AC018437 Homo sapiens chromosome 8, clone RP11-77B22, complete sequence
515	CP119128 <i>Sphingobium</i> sp. WTD-1 plasmid unnamed1, complete sequence
515	AC105763 Homo sapiens BAC clone RP11-698H21 from 4, complete sequence
514	XR_007063212 PREDICTED: Homo sapiens uncharacterized LOC124902879 (LOC124902879), ncRNA
514	AL583827 Human DNA sequence from clone RP11-172F7 on chromosome 9, complete sequence
514	AL356473 Human DNA sequence from clone RP11-560O20 on chromosome 6, complete sequence
512	AC079269 Homo sapiens chromosome 10 clone RP11-379L21, complete sequence
512	AC009498 Homo sapiens BAC clone RP11-507C18 from 2, complete sequence
512	AL355333 Human DNA sequence from clone RP11-575N15 on chromosome 10, complete sequence
512	AP001827 Homo sapiens genomic DNA, chromosome 11 clone:RP11-236L10, complete sequence
510	AY623111 Homo sapiens CDC14 cell division cycle 14 homolog A (<i>S. cerevisiae</i>) (CDC14A) gene, complete
510	AC013725 Homo sapiens BAC clone RP11-323F5 from 4, complete sequence
509	NG_011994 Homo sapiens phosphodiesterase 7B (PDE7B), RefSeqGene on chromosome 6
507	AC104373 Homo sapiens chromosome 8, clone RP11-1144P22, complete sequence
507	CU463228 Human DNA sequence from clone XX-NCIH1770_2K21, complete sequence
507	XR_007068344 PREDICTED: Homo sapiens uncharacterized LOC124905222 (LOC124905222), ncRNA
507	AC125245 Homo sapiens BAC clone RP11-236P13 from 4, complete sequence
506	AC225619 Homo sapiens FOSMID clone ABC14-50461600B11 from chromosome 1, complete sequence
505	AC022224 Homo sapiens 12p BAC RP11-248B13 (Roswell Park Cancer Institute Human BAC Library) complete
505	AL031985 Human DNA sequence from clone RP1-228H13 on chromosome 1p34.1-35.3, complete sequence
505	AC009743 Homo sapiens 3 BAC RP11-372H2 (Roswell Park Cancer Institute Human BAC Library) complete se
504	AC104780 Homo sapiens BAC clone RP11-27N13 from 2, complete sequence
504	AC021621 Homo sapiens chromosome 8, clone RP11-356M23, complete sequence
503	CP116005 <i>Sphingosinicella microcystinivorans</i> strain DMF-3 chromosome, complete genome
503	CP046565 <i>Methylococcus geothermalis</i> strain IM1 chromosome, complete genome
503	AP003025 Homo sapiens genomic DNA, chromosome 11q, clone:RP11-217L21, complete sequence
503	AC008664 Homo sapiens chromosome 5 clone CTB-34B5, complete sequence

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
503	AL138836 Human DNA sequence from clone RP11-88M19 on chromosome 9, complete sequence
502	CP050223 Mycobacteroides chelonae strain Myco1 chromosome
502	AL022098 Human DNA sequence from clone RP3-510L9 on chromosome 6p24.1-25.3, complete sequence
501	CP029344 Hydrogenophaga sp. NH-16 chromosome
501	NG_011487 Homo sapiens membrane associated guanylate kinase, WW and PDZ domain containing 2 (MAGI2)
501	NG_046919 Homo sapiens neuroligin 1 (NLGN1), RefSeqGene on chromosome 3
500	CP002665 Cellulomonas gilvus ATCC 13127 chromosome, complete genome
500	BC050676 Homo sapiens hypothetical protein MGC5242, mRNA (cDNA clone IMAGE:6043548), partial cds
500	AC270515 Homo sapiens chromosome 7 clone CH17-202E11, complete sequence
499	AC093889 Homo sapiens BAC clone RP11-671G14 from 7, complete sequence
498	AC018887 Homo sapiens BAC clone RP11-419E14 from 2, complete sequence
498	AL445663 Human DNA sequence from clone RP11-442A13 on chromosome 9, complete sequence
498	CP071632 Rhizobium sp. NZLR1 chromosome, complete genome
497	CP020553 Staphylococcus aureus strain SA112 chromosome
497	CP029761 Sphingomonas sp. IC081 chromosome C1, complete sequence
497	CP085618 Xanthobacter autotrophicus strain GJ10 chromosome
497	NG_008972 Homo sapiens decaprenyl diphosphate synthase subunit 1 (PDSS1), RefSeqGene on chromosome
497	NG_032064 Homo sapiens dolichyl-diphosphooligosaccharide-protein glycosyltransferase non-catalytic
496	AC013283 Homo sapiens 12 BAC RP11-481K9 (Roswell Park Cancer Institute Human BAC Library) complete s
496	AC079054 Homo sapiens chromosome 8, clone RP11-158A14, complete sequence
496	NG_012107 Homo sapiens opioid binding protein/cell adhesion molecule like (OPCML), RefSeqGene on ch
495	AL356288 Human DNA sequence from clone RP11-6E3 on chromosome 1, complete sequence
495	CP079203 Sphingomonas sanguinis strain NP2-R2 chromosome, complete genome
495	AP001891 Homo sapiens genomic DNA, chromosome 11q, clone:RP11-356E17, complete sequence
495	XR_007076969 PREDICTED: Homo sapiens uncharacterized LOC124901360 (LOC124901360), ncRNA
495	AC270160 Homo sapiens BAC clone CH17-340J7 from chromosome unknown, complete sequence
494	CP022751 Sphingobium xenophagum strain C1 plasmid p5, complete sequence
494	AC010197 Homo sapiens 12p12p11-37.2-54.4 BAC RP11-92H16 (Roswell Park Cancer Institute Human BAC Lib
494	AC096718 Homo sapiens BAC clone RP11-10P19 from 4, complete sequence
493	AP024048 Homo sapiens DNA, sequence_id: unplaced_0563
493	CP053553 Diaphorobacter sp. JS3050 chromosome, complete genome
493	OK649235 Homo sapiens cell line MHC_QBL major histocompatibility complex genomic sequence
492	AC104434 Homo sapiens chromosome 3 clone RP11-625B23, complete sequence
492	NG_033785 Homo sapiens collagen type XXVI alpha 1 chain (COL26A1), RefSeqGene on chromosome 7
492	NG_084706 Homo sapiens CDK7 strongly-dependent group 2 enhancer GRCh37_chr7:141645256-141646455 (L
492	CP047895 Sphingomonas changnyeongensis strain C33 chromosome, complete genome
492	AP000787 Homo sapiens genomic DNA, chromosome 11 clone:RP11-712B9, complete sequence
492	AC279073 Homo sapiens chromosome 16 clone VMRC59-122D16, complete sequence
492	NG_012232 Homo sapiens dystrophin (DMD), RefSeqGene (LRG_199) on chromosome X
491	AF286887 Homo sapiens chromosome 8 clone RP11-206N20 map q12.1, complete sequence
491	AC090001 Homo sapiens 12 BAC RP11-536G4 (Roswell Park Cancer Institute Human BAC Library) complete s
491	AL590115 Human DNA sequence from clone RP11-255O17 on chromosome 1, complete sequence
490	CP117028 Sphingomonas hankookensis strain SZ.B2R2 plasmid pSZ.B2R2_3, complete sequence
490	NG_012827 Homo sapiens contactin 4 (CNTN4), RefSeqGene on chromosome 3
490	AF216671 Homo sapiens chromosome 8 clone RP11-300I14 map q24.13, complete sequence
490	AL445932 Human DNA sequence from clone RP11-533L1 on chromosome 6, complete sequence
490	NM_002585 Homo sapiens PBX homeobox 1 (PBX1), transcript variant 1, mRNA
490	NG_046773 Homo sapiens coiled-coil domain containing 174 (CCDC174), RefSeqGene on chromosome 3
489	CP023704 Caldicoccus thermoamylovorans strain SSBM chromosome, complete genome
489	CP009291 Novosphingobium pentaromativorans US6-1, complete genome
489	NG_023204 Homo sapiens solute carrier family 6 member 20 (SLC6A20), RefSeqGene on chromosome 3
489	AC012066 Homo sapiens BAC clone RP11-173H9 from 2, complete sequence
488	CP021024 Rhizobium sp. TAL182 chromosome, complete genome
488	NM_004196 Homo sapiens cyclin dependent kinase like 1 (CDKL1), transcript variant 1, mRNA

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
487	AP023493 Homo sapiens DNA, sequence_id: unplaced_0008
487	AC024255 Homo sapiens 12 BAC RP11-31A23 (Roswell Park Cancer Institute Human BAC Library) complete s
487	NG_042292 Homo sapiens potassium voltage-gated channel subfamily A regulatory beta subunit 1 (KCNA
487	AC022858 Homo sapiens chromosome 8, clone RP11-326E22, complete sequence
487	NG_030020 Homo sapiens dihydropyrimidinase like 2 (DPYSL2), RefSeqGene on chromosome 8
487	AC074045 Homo sapiens Xp BAC RP11-60N3 (Roswell Park Cancer Institute Human BAC Library) complete se
487	CP025934 Cutibacterium acnes DSM 1897 chromosome, complete genome
486	AC107219 Homo sapiens BAC clone RP11-575B4 from 4, complete sequence
486	AC270241 Homo sapiens BAC clone CH17-338K16 from chromosome 7, complete sequence
486	AP001284 Homo sapiens genomic DNA, chromosome 11 clone:RP11-885L14, complete sequence
486	CP048420 Sphingomonas insulae strain KCTC 12872 plasmid unnamed2, complete sequence
485	AL157782 Human DNA sequence from clone RP11-127E22 on chromosome 10, complete sequence
485	AC002465 Homo sapiens BAC clone CTA-343P13 from 7, complete sequence
485	AC280089 Homo sapiens chromosome unknown clone VMRC69-204K20, complete sequence
484	AC096736 Homo sapiens BAC clone RP11-171N4 from 4, complete sequence
484	AP003068 Homo sapiens genomic DNA, chromosome 11 clone:RP11-399J13, complete sequence
483	AF235096 Homo sapiens chromosome 8 clone RP11-562D1 map q24.13, complete sequence
483	AC024192 Homo sapiens BAC clone RP11-476H13 from 4, complete sequence
483	AC229651 Homo sapiens FOSMID clone ABC14-50153500N23 from chromosome unknown, complete sequence
483	AC114947 Homo sapiens chromosome 5 clone CTD-2636A23, complete sequence
483	NG_021864 Homo sapiens nicotinamide phosphoribosyltransferase pseudogene 2 (NAMPTP2) on chromosome
482	CP039352 Vigna unguiculata cultivar Xiabao 2 chromosome Vu10
482	AL137783 Human DNA sequence from clone RP5-1181K21 on chromosome 6, complete sequence
482	AC009785 Homo sapiens chromosome 7 clone RP11-198E23, complete sequence
482	AC006042 Homo sapiens BAC clone RP11-505D17 from 7, complete sequence
481	AC079015 Homo sapiens chromosome 8, clone RP11-489O18, complete sequence
481	AP022845 Cutibacterium acnes S22 DNA, complete genome
481	AL358134 Human DNA sequence from clone RP11-306O13 on chromosome 6, complete sequence
481	NG_011965 Homo sapiens mitogen-activated protein kinase kinase kinase 5 (MAP3K5), RefSeqGene on chr
481	AC255533 Homo sapiens chromosome 6 clone CH17-298E21, complete sequence
480	CP024314 Rhizobium sp. NXC24 plasmid pRspNXC24c, complete sequence
480	OK649233 Homo sapiens cell line MHC_KAS116 major histocompatibility complex genomic sequence
480	CP032345 Azospirillum brasilense strain MTCC4039 chromosome, complete genome
480	NG_029800 Homo sapiens laminin subunit gamma 3 (LAMC3), RefSeqGene on chromosome 9
480	NG_015822 Homo sapiens ligand dependent nuclear receptor corepressor like (LCORL), RefSeqGene on ch
480	NG_051023 Homo sapiens LDL receptor related protein 1B (LRP1B), RefSeqGene on chromosome 2
479	CP006644 Sphingomonas sanxanigenens NX02, complete genome
479	AC096653 Homo sapiens BAC clone RP11-16P17 from 4, complete sequence
479	AP003078 Homo sapiens genomic DNA, chromosome 11q clone:CTD-2504H21, complete sequence
479	AC110072 Homo sapiens BAC clone RP11-18C16 from 4, complete sequence
478	NG_053082 Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), RefSeqGene on chromos
478	AL117373 Human DNA sequence from clone RP5-1188A21 on chromosome 6q22.32-22.3, complete sequence
478	AC096556 Homo sapiens BAC clone RP11-102G8 from 2, complete sequence
478	AL355499 Human DNA sequence from clone RP11-328K6 on chromosome 6, complete sequence
478	AC113398 Homo sapiens chromosome 5 clone RP11-436H11, complete sequence
478	AB041511 Homo sapiens genomic DNA, chromosome 6q21, clone:57112, complete sequence
478	AL355532 Human DNA sequence from clone RP11-487F5 on chromosome 6 Contains the 3' part of the GRIK2
478	CP078509 Stutzerimonas stutzeri strain S116 chromosome, complete genome
478	AY523969 Homo sapiens catenin (cadherin-associated protein), alpha-like 1 (CTNNA1) gene, complete c
478	CP034510 Eukaryotic synthetic construct chromosome Y
478	NG_029042 Homo sapiens prolactin receptor (PRLR), RefSeqGene on chromosome 5; nuclear gene for mito
477	AC243269 Homo sapiens FOSMID clone ABC8-5708749H18 from chromosome x, complete sequence
477	AC068492 Homo sapiens BAC clone RP11-809C23 from 2, complete sequence
477	AC006226 Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
477	AC022731 Homo sapiens chromosome 8, clone RP11-382J12, complete sequence
477	AL450307 Human DNA sequence from clone RP11-245K15 on chromosome 10, complete sequence
477	NG_013375 Homo sapiens lemur tyrosine kinase 2 (LMTK2), RefSeqGene on chromosome 7
476	AL136122 Human DNA sequence from clone RP3-413L20 on chromosome 6, complete sequence
476	AC016682 Homo sapiens BAC clone RP11-62P16 from 2, complete sequence
476	AC010252 Homo sapiens chromosome 5 clone CTC-428I3, complete sequence
476	AC012513 Homo sapiens BAC clone RP11-566E18 from 2, complete sequence
476	AC234317 Homo sapiens FOSMID clone ABC14-50086100A18 from chromosome 4, complete sequence
476	AC006994 Homo sapiens BAC clone RP11-396J8 from 2, complete sequence
476	AC115283 Homo sapiens chromosome 3 clone RP11-632K8, complete sequence
475	AC104246 Homo sapiens chromosome 8, clone RP11-1073L1, complete sequence
475	AC245605 Homo sapiens FOSMID clone COR2A-DD0002TIHNU_L6 from chromosome 6, complete sequence
474	AC022535 Homo sapiens chromosome 10 clone RP11-34C15, complete sequence
474	NG_008899 Homo sapiens sarcoglycan zeta (SGCZ), RefSeqGene (LRG_208) on chromosome 8
474	AL009177 Human DNA sequence from clone RP3-365E2 on chromosome 6p22.3-24.1, complete sequence
474	AB073353 Homo sapiens primary neuroblastoma cDNA, clone:Nbla03526, full insert sequence
474	AC116442 Homo sapiens chromosome 3 clone RP11-534H12, complete sequence
474	AC019057 Homo sapiens BAC clone RP11-121A1 from 2, complete sequence
473	OD957125 Naegleria fowleri Karachi_NF001 strain
473	AC008171 Homo sapiens BAC clone RP11-326D7 from 2, complete sequence
473	CP044125 Rhizobium sp. BG4 chromosome, complete genome
473	NG_011878 Homo sapiens neurexin 1 (NRXN1), RefSeqGene on chromosome 2
473	AL607076 Human DNA sequence from clone RP11-321J5 on chromosome 10, complete sequence
473	XM_054326057 PREDICTED: Homo sapiens kelch like family member 22 (KLHL22), transcript variant X1, m
472	CP098764 Sphingomonas aerolata strain PDD-32b-11 plasmid unnamed2, complete sequence
472	AP023477 Homo sapiens DNA, chromosome 17, nearly complete genome
472	CP060494 Sphingosinithalassobacter sp. CS137 chromosome, complete genome
472	AC009308 Homo sapiens BAC clone RP11-299P22 from 7, complete sequence
472	AC067956 Homo sapiens BAC clone RP11-140F14 from 2, complete sequence
472	NG_011538 Homo sapiens potassium voltage-gated channel interacting protein 1 (KCINP1), RefSeqGene o
471	CP130791 Mycobacterium tuberculosis strain MTb-Oman-3213249 chromosome, complete genome
471	AC093730 Homo sapiens BAC clone RP11-12K22 from 4, complete sequence
471	AC002386 Homo sapiens BAC clone CTA-343H22 from 7, complete sequence
470	AL357619 Human DNA sequence from clone RP11-703H16 on chromosome 6, complete sequence
470	XM_054320750 PREDICTED: Homo sapiens glutamate ionotropic receptor kainate type subunit 5 (GRIK5),
469	CP068260 Homo sapiens isolate CHM13 chromosome 18
469	KX265236 Homo sapiens erythroblast membrane-associated protein (ERMAP) gene, ERMAP-002 allele, compl
469	AC278331 Homo sapiens chromosome 7 clone VMRC62-404M06, complete sequence
469	AC093767 Homo sapiens BAC clone RP11-107E21 from 4, complete sequence
469	NG_033948 Homo sapiens lysine methyltransferase 2C (KMT2C), RefSeqGene on chromosome 7
469	AC004906 Homo sapiens PAC clone RP5-852O24 from 7, complete sequence
468	AC131572 Homo sapiens chromosome 11, clone RP11-496I9, complete sequence
468	AC099790 Homo sapiens chromosome 1 clone RP11-397G23, complete sequence
468	CP101740 Sphingomonas qomolangmaensis strain S5-59 chromosome, complete genome
468	AC016950 Homo sapiens 3 BAC RP11-239I11 (Roswell Park Cancer Institute Human BAC Library) complete s
468	NG_011877 Homo sapiens reelin (RELN), RefSeqGene on chromosome 7
468	AC108141 Homo sapiens BAC clone RP11-400H15 from 4, complete sequence
468	AL831755 Human DNA sequence from clone RP13-279N23 on chromosome 1, complete sequence
468	AL357041 Human DNA sequence from clone RP11-221L2 on chromosome 1, complete sequence
468	AC112255 Homo sapiens BAC clone RP11-1193F23 from 2, complete sequence
468	AC100798 Homo sapiens chromosome 8, clone RP11-600K15, complete sequence
468	AC277738 Homo sapiens chromosome 1 clone VMRC69-45A14, complete sequence
468	AC099501 Homo sapiens chromosome 5 clone RP11-200I3, complete sequence
467	AP024005 Homo sapiens DNA, sequence_id: unplaced_0520

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
467	AC226113 Homo sapiens FOSMID clone ABC12-49050600E21 from chromosome 7, complete sequence
466	KT331523 Macaca mulatta isolate Rh24400_6332-3a major histocompatibility complex genomic sequence
466	XM_054372529 PREDICTED: Homo sapiens fatty acyl-CoA reductase 2 (FAR2), transcript variant X2, mRNA
466	KC951431 Homo sapiens clone FOS_0066, complete sequence
466	AC107056 Homo sapiens BAC clone RP11-464N24 from 4, complete sequence
466	AC099497 Homo sapiens chromosome 5 clone RP11-139A10, complete sequence
466	AC068050 Homo sapiens BAC clone RP11-240E2 from 9, complete sequence
466	AL365254 Human DNA sequence from clone RP11-420H21 on chromosome 1, complete sequence
466	AC010255 Homo sapiens chromosome 5 clone CTC-441N14, complete sequence
466	CP050265 MAG: Erythrobacter sp. isolate NP_1 chromosome, complete genome
465	AL356258 Human DNA sequence from clone RP11-170J4 on chromosome 10, complete sequence
465	AC006253 Homo sapiens 3p22-8 PAC RPC15-1033M1 (Roswell Park Cancer Institute Human PAC Library) comp
465	AC004863 Homo sapiens PAC clone RP4-708P22 from 7, complete sequence
465	CP065666 Acinetobacter johnsonii strain FDAARGOS_910 chromosome, complete genome
465	AC092803 Homo sapiens chromosome 1 clone RP11-61J19, complete sequence
465	AL353769 Human DNA sequence from clone RP11-188L14 on chromosome 10, complete sequence
465	CP038203 Paracoccus pantotrophus strain DSM 11072 chromosome, complete genome
464	CP049107 Rhizorhabdus phycosphaerae strain MK52 chromosome, complete genome
464	AL157883 Human DNA sequence from clone RP11-360J12 on chromosome 9q21.12-21.32, complete sequence
464	AC005095 Homo sapiens BAC clone CTA-332P12 from 7q22-q31.1, complete sequence
464	AC021856 Homo sapiens BAC clone RP11-553E5 from 4, complete sequence
464	AC068522 Homo sapiens chromosome 8, clone RP11-23K11, complete sequence
464	KY500878 Homo sapiens isolate WT51 NOTCH4 gene, complete cds
464	AC239612 Homo sapiens BAC clone RP11-654L23 from chromosome 7, complete sequence
464	AC073968 Homo sapiens BAC clone RP11-111G20 from 7, complete sequence
464	CP044074 Pseudomonas oryzae strain FDAARGOS_657 chromosome, complete genome
464	AC093326 Homo sapiens BAC clone RP11-625N16 from 2, complete sequence
464	DQ070893 Homo sapiens AGR2 (AGR2) gene, complete cds, alternatively spliced
464	AC103834 Homo sapiens chromosome 8, clone RP11-1081K18, complete sequence
464	AC092372 Homo sapiens chromosome 5 clone RP11-58M12, complete sequence
463	NG_008194 Homo sapiens lipase A, lysosomal acid type (LIPA), RefSeqGene on chromosome 10
463	AP000797 Homo sapiens genomic DNA, chromosome 11 clone:CMB9-36B5, complete sequence
463	AC090719 Homo sapiens chromosome 11, clone RP11-648B16, complete sequence
463	AC279079 Homo sapiens chromosome 17 clone VMRC59-182E09, complete sequence
463	NG_016983 Homo sapiens kelch like family member 7 (KLHL7), RefSeqGene on chromosome 7
462	CP053903 Mycobacterium tuberculosis strain H37Rv_IC1 chromosome
462	AC112719 Homo sapiens BAC clone RP11-630D6 from 4, complete sequence
462	AL359273 Human DNA sequence from clone RP11-376N17 on chromosome 1, complete sequence
462	AP001930 Homo sapiens genomic DNA, chromosome 11q clone:RP11-669L23, complete sequences
462	AC011419 Homo sapiens chromosome 5 clone CTD-2029I9, complete sequence
462	AP000841 Homo sapiens genomic DNA, chromosome 11q clone:CMB9-89J9, complete sequence
461	CP119314 MAG: Sphingomonas sp. isolate MAG 3606 chromosome, complete genome
461	AL445426 Human DNA sequence from clone RP11-62J10 on chromosome 1, complete sequence
461	CP026100 Caulobacter flavus strain RHGG3 chromosome, complete genome
461	NG_051226 Homo sapiens basophilin 2 (BNC2), RefSeqGene on chromosome 9
461	AC270292 Homo sapiens chromosome 8 clone CH17-294L6, complete sequence
461	CP073095 Corynebacterium tuberculoostearicum strain CTNIH10 chromosome, complete genome
461	CP065592 Sphingosinicella flava strain UDD2 chromosome
460	AP023859 Homo sapiens DNA, sequence_id: unplaced_0374
460	AC092933 Homo sapiens 3 BAC RP11-200I19 (Roswell Park Cancer Institute Human BAC Library) complete s
460	NG_051831 Homo sapiens gamma-aminobutyric acid type A receptor subunit beta1 (GABRB1), RefSeqGene o
460	AL645616 Human DNA sequence from clone RP11-16O14 on chromosome 10, complete sequence
460	AC009365 Homo sapiens chromosome 7 clone RP11-355K3, complete sequence
460	CP069568 Corynebacterium sp. FDAARGOS 1242 strain FDAARGOS_1242 chromosome, complete genome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
459	AC073612 Homo sapiens 12 BAC RP11-293I14 (Roswell Park Cancer Institute Human BAC Library) complete
459	AC006502 Homo sapiens, clone hRPK.36_A_1, complete sequence
458	MN849867 Homo sapiens isolate PNG98 haplogroup B4a1a1a mitochondrion, complete genome
458	MK279922 Homo sapiens lncAB599.2 lncRNA gene, complete sequence
458	AC025448 Homo sapiens chromosome 5 clone CTD-2113L7, complete sequence
458	NG_054744 Homo sapiens semaphorin 3C (SEMA3C), RefSeqGene on chromosome 7
458	NG_029966 Homo sapiens protein tyrosine phosphatase receptor type N2 (PTPRN2), RefSeqGene on chromo
458	AL360004 Human DNA sequence from clone RP11-88G17 on chromosome 9, complete sequence
458	CP033150 Malassezia restricta CBS 7877 chromosome III
458	NG_033950 Homo sapiens adhesion G protein-coupled receptor L3 (ADGRL3), RefSeqGene on chromosome 4
458	AL354712 Human DNA sequence from clone RP4-597A16 on chromosome 1p36.13-36.23, complete sequence
457	CP054031 Rhizobium indicum strain JKLM 13E chromosome, complete genome
457	AP003470 Homo sapiens genomic DNA, chromosome 8q23, clone: KB1460A12
457	AC097461 Homo sapiens BAC clone RP11-16P6 from 2, complete sequence
457	NG_023443 Homo sapiens eyes shut homolog (EYS), RefSeqGene on chromosome 6
457	NG_053151 Homo sapiens ankyrin repeat domain 31 (ANKRD31), RefSeqGene on chromosome 5
456	CP053021 Sphingobium yanoikuyae strain YC-XJ2 chromosome, complete genome
456	AC079921 Homo sapiens BAC clone RP11-360F5 from 4, complete sequence
456	NG_042093 Homo sapiens lysine acetyltransferase 6A (KAT6A), RefSeqGene on chromosome 8
456	NG_015799 Homo sapiens phospholipase C epsilon 1 (PLCE1), RefSeqGene on chromosome 10
455	BA000012 Mesorhizobium loti MAFF303099 DNA, complete genome
455	NG_009224 Homo sapiens glutamate ionotropic receptor kainate type subunit 2 (GRIK2), RefSeqGene on
455	NG_034039 Homo sapiens dedicator of cytokinesis 10 (DOCK10), RefSeqGene on chromosome 2
455	NG_017198 Homo sapiens Rho guanine nucleotide exchange factor 28 (ARHGEF28), RefSeqGene on chromoso
455	AL731573 Human DNA sequence from clone RP11-215C13 on chromosome 10, complete sequence
455	AL031767 Human DNA sequence from clone RP1-135L22 on chromosome 6p22.2-22.3, complete sequence
455	CP017637 Bradyrhizobium japonicum strain J5 chromosome, complete genome
455	AC279486 Homo sapiens chromosome unknown clone VMRC59-228P04, complete sequence
454	NG_011571 Homo sapiens ataxin 1 (ATXN1), RefSeqGene (LRG_863) on chromosome 6
454	AC105937 Homo sapiens chromosome 3 clone RP11-45J19, complete sequence
454	AC110000 Homo sapiens chromosome 5 clone CTD-2553C14, complete sequence
454	AC007240 Homo sapiens BAC clone RP11-83M8 from 2, complete sequence
454	AC011741 Homo sapiens BAC clone RP11-113E4 from 2, complete sequence
453	AC004854 Homo sapiens PAC clone RP4-673M15 from 7, complete sequence
453	AC005037 Homo sapiens BAC clone RP11-469M7 from 2, complete sequence
453	NG_029612 Homo sapiens SRY-box transcription factor 5 (SOX5), RefSeqGene on chromosome 12
452	AP023479 Homo sapiens DNA, chromosome 19, nearly complete genome
452	XM_054371052 PREDICTED: Homo sapiens leucine rich repeat kinase 2 (LRRK2), transcript variant X5, m
452	NG_044232 Homo sapiens thioesterase superfamily member 7, pseudogene (THEM7P) on chromosome 11
452	MN298073 Homo sapiens LHRI_LNC914.1 lncRNA gene, complete sequence
452	AL451185 Human DNA sequence from clone RP11-136C6 on chromosome 6, complete sequence
452	AC010455 Homo sapiens chromosome 5 clone CTD-2255G13, complete sequence
452	NM_012254 Homo sapiens solute carrier family 27 member 5 (SLC27A5), transcript variant 1, mRNA
452	CP068206 Acinetobacter johnsonii strain FDAARGOS_1092 chromosome, complete genome
452	NR_109846 Homo sapiens potassium voltage-gated channel subfamily A member 3 (KCNA3), transcript var
452	NG_051945 Homo sapiens solute carrier family 6 member 17 (SLC6A17), RefSeqGene on chromosome 1
452	AC083949 Homo sapiens BAC clone CTD-2096A9 from 2, complete sequence
451	AL357141 Human DNA sequence from clone RP11-702N8 on chromosome 6, complete sequence
451	AC277917 Homo sapiens chromosome 1 clone CH17-39E12, complete sequence
451	AP001939 Homo sapiens genomic DNA, chromosome 4q22-q24, clone:2231G18, complete sequence
451	AC016737 Homo sapiens BAC clone RP11-394I13 from 2, complete sequence
451	AC011726 Homo sapiens chromosome , clone RP11-141I7, complete sequence
451	AC225602 Homo sapiens FOSMID clone ABC12-46837000B2 from chromosome unknown, complete sequence
451	AL596225 Human DNA sequence from clone RP11-30D7 on chromosome 1, complete sequence

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
451	NG_028077 Homo sapiens shroom family member 3 (SHROOM3), RefSeqGene on chromosome 4
451	AC103560 Homo sapiens chromosome 3 clone RP11-673E20, complete sequence
450	AP003399 Homo sapiens genomic DNA, chromosome 11q clone:RP11-448N3, complete sequence
450	AL589943 Human DNA sequence from clone RP11-44D23 on chromosome 10, complete sequence
450	AC015542 Homo sapiens 3 BAC RP11-38B6 (Roswell Park Cancer Institute Human BAC Library) complete seq
450	NG_015963 Homo sapiens EGF like domain multiple 6 (EGFL6), RefSeqGene on chromosome X
450	AC016764 Homo sapiens BAC clone RP11-549G13 from 2, complete sequence
450	AC012464 Homo sapiens 12 BAC RP11-1060G2 (Roswell Park Cancer Institute Human BAC Library) complete
449	AC098931 Homo sapiens chromosome 3 clone RP11-353I6, complete sequence
449	AC099515 Homo sapiens chromosome 5 clone RP11-455D3, complete sequence
449	AC091836 Homo sapiens chromosome 5 clone CTD-2060B6, complete sequence
449	AL158823 Human DNA sequence from clone RP11-151F5 on chromosome 9, complete sequence
449	EF015899 Homo sapiens photolyase-like cryptochrome 2 (CRY2) gene, complete cds
449	AC008929 Homo sapiens chromosome 5, complete sequence
449	AC068134 Homo sapiens BAC clone RP11-762N20 from 2, complete sequence
449	AC215296 Homo sapiens FOSMID clone ABC9-44016800J15 from chromosome 2, complete sequence
448	CP021181 Rhizorhabdus wittichii DC-6 chromosome, complete genome
448	AC073896 Homo sapiens 12 BAC RP11-977G19 (Roswell Park Cancer Institute Human BAC Library) complete
448	AC213291 Homo sapiens chromosome 6 clone ABC8_000000738440_L11, complete sequence
448	AC103816 Homo sapiens chromosome 8, clone CTC-497K19, complete sequence
448	AC015687 Homo sapiens chromosome , clone RP11-18M5, complete sequence
448	AC009731 Homo sapiens 12 BAC RP11-438N16 (Roswell Park Cancer Institute Human BAC Library) complete
448	AL359963 Human DNA sequence from clone RP11-18A3 on chromosome 9, complete sequence
448	AC025155 Homo sapiens 3 BAC RP11-487M24 (Roswell Park Cancer Institute Human BAC Library) complete s
448	AL133552 Human DNA sequence from clone RP11-67B16 on chromosome 10, complete sequence
447	NG_029476 Homo sapiens cut like homeobox 1 (CUX1), RefSeqGene (LRG_1123) on chromosome 7
447	AC106867 Homo sapiens BAC clone RP11-162F1 from 4, complete sequence
447	AC087521 Homo sapiens chromosome 11, clone RP11-613D13, complete sequence
447	AC010136 Homo sapiens BAC clone RP11-129D2 from 2, complete sequence
446	NG_008860 Homo sapiens nibrin (NBN), RefSeqGene (LRG_158) on chromosome 8
446	AC105765 Homo sapiens chromosome 3 clone RP11-54L6, complete sequence
446	AC093753 Homo sapiens BAC clone RP11-50C12 from 4, complete sequence
446	AC279081 Homo sapiens chromosome 16 clone VMRC59-219L03, complete sequence
446	NG_032977 Homo sapiens interleukin 12 receptor subunit beta 2 (IL12RB2), RefSeqGene (LRG_707) on c
446	AC026124 Homo sapiens 12 BAC RP11-305O6 (Roswell Park Cancer Institute Human BAC Library) complete s
446	AC109445 Homo sapiens chromosome 5 clone CTD-2351A8, complete sequence
445	CP025935 Cutibacterium acnes KPA171202 chromosome, complete genome
445	NG_021366 Homo sapiens NPSR1 antisense RNA 1 (NPSR1-AS1), RefSeqGene on chromosome 7
445	AC008176 Homo sapiens BAC clone RP11-451F11 from 7p11.2-p21, complete sequence
445	NG_029494 Homo sapiens diacylglycerol kinase beta (DGKB), RefSeqGene on chromosome 7
445	AP002353 Homo sapiens genomic DNA, chromosome 11 clone:CTD-2651C21, complete sequence
444	AC020637 Homo sapiens 12 BAC RP11-530H22 (Roswell Park Cancer Institute Human BAC Library) complete
444	AC132807 Homo sapiens chromosome 3 clone RP11-147G2, complete sequence
444	AC005079 Homo sapiens BAC clone CTA-252P22 from 7, complete sequence
444	AC242869 Homo sapiens FOSMID clone ABC12-47017600C13 from chromosome 6, complete sequence
444	AC027119 Homo sapiens chromosome 3 clone RP11-113L10 map 3p, complete sequence
444	AL512368 Human DNA sequence from clone RP11-387L5 on chromosome 6, complete sequence
443	NG_013376 Homo sapiens palladin, cytoskeletal associated protein (PALLD), RefSeqGene on chromosome
443	CP027242 Peptostreptococcaceae bacterium oral taxon 929 strain W2294 chromosome, complete genome
443	AP002453 Homo sapiens genomic DNA, chromosome 11 clone:RP11-801G16, complete sequence
443	NG_046914 Homo sapiens DAB adaptor protein 1 (DAB1), RefSeqGene on chromosome 1; nuclear gene for m
443	AC092709 Homo sapiens chromosome 8, clone RP11-509P12, complete sequence
443	AC105387 Homo sapiens BAC clone RP11-163N10 from 4, complete sequence
443	AC103716 Homo sapiens chromosome 8, clone RP11-344I13, complete sequence

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
442	NG_012150 Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 2 (PAPSS2), RefSeqGene on chr
442	CP053344 Herbiconiux sp. SALV-R1 chromosome, complete genome
442	AL513320 Human DNA sequence from clone RP11-46F15 on chromosome 1, complete sequence
442	AC015509 Homo sapiens chromosome 8, clone RP11-21M19, complete sequence
442	AL831782 Human DNA sequence from clone RP4-636P16 on chromosome 1, complete sequence
442	AC022260 Homo sapiens chromosome 8, clone RP11-426C8, complete sequence
442	NG_029677 Homo sapiens glutamate metabotropic receptor 4 (GRM4), RefSeqGene on chromosome 6
442	CP011515 Mitsuraria sp. 7 plasmid, complete sequence
441	AP024056 Homo sapiens DNA, sequence_id: unplaced_0571
441	XM_047444311 PREDICTED: Homo sapiens ubiquitin carboxyl-terminal hydrolase 17-like protein 22 (LOC1
441	CP039355 Vigna unguiculata cultivar Xiabao 2 chromosome Vu09
441	AC079809 Homo sapiens BAC clone RP11-958M14 from 7, complete sequence
441	AC279094 Homo sapiens chromosome 17 clone VMRC59-275N16, complete sequence
441	AL513412 Homo sapiens chromosome 9 BAC RP11-403H13, complete sequence
441	CP061177 Roseomonas haemaphysalidis strain 546 chromosome, complete genome
441	AC011739 Homo sapiens BAC clone RP11-68H19 from 2, complete sequence
441	AL590094 Human DNA sequence from clone RP11-233A23 on chromosome 1, complete sequence
441	AL593854 Human DNA sequence from clone RP11-423B13 on chromosome 6, complete sequence
441	AC233296 Homo sapiens BAC clone RP11-761A18 from chromosome x, complete sequence
441	AC012445 Homo sapiens BAC clone RP11-86A21 from 2, complete sequence
441	AC105081 Homo sapiens chromosome 8, clone CTC-788C1, complete sequence
441	AC239643 Homo sapiens FOSMID clone COR2A-DD0002R6SNU_F13 from chromosome 7, complete sequence
441	AC110078 Homo sapiens BAC clone RP11-358N5 from 2, complete sequence
441	AL139300 Human chromosome 14 DNA sequence BAC R-894P9 of library RPCI-11 from chromosome 14 of Homo
441	AC241670 Homo sapiens FOSMID clone ABC11-47211400H13 from chromosome 6, complete sequence
440	NC_049392 Escherichia phage ESSi2_ev239 genome assembly, chromosome: 1
440	AC073464 Homo sapiens BAC clone RP11-134N21 from 2, complete sequence
440	AC093295 Homo sapiens chromosome 5 clone RP11-535A15, complete sequence
440	AC096549 Homo sapiens BAC clone RP11-5K15 from 2, complete sequence
440	AC068721 Homo sapiens BAC clone RP11-545L5 from 4, complete sequence
440	AF216667 Homo sapiens chromosome 8 clone CTC-543J1 map 8q24.3, complete sequence.
440	AC026421 Homo sapiens chromosome 5 clone CTD-2127O16, complete sequence
439	AP000789 Homo sapiens genomic DNA, chromosome 11 clone:RP11-725K16, complete sequence
439	CP068259 Homo sapiens isolate CHM13 chromosome 19
439	AL589684 Human DNA sequence from clone RP11-437J19 on chromosome 6, complete sequence
439	AC004990 Homo sapiens PAC clone RP5-1185I7 from 7, complete sequence
439	AC067849 Homo sapiens chromosome 8, clone RP11-709L14, complete sequence
439	AC090015 Homo sapiens 12 BAC RP11-711C17 (Roswell Park Cancer Institute Human BAC Library) complete
439	NG_054895 Homo sapiens cysteine rich hydrophobic domain 1 (CHIC1), RefSeqGene on chromosome X
439	AC016920 Homo sapiens 3 BAC RP11-203L15 (Roswell Park Cancer Institute Human BAC Library) complete s
439	AC010493 Homo sapiens chromosome 5 clone CTD-2347I17, complete sequence
439	AL353681 Human DNA sequence from clone RP1-158P9 on chromosome 1, complete sequence
439	AL591178 Human DNA sequence from clone RP11-293P20 on chromosome 1, complete sequence
438	AC007403 Homo sapiens BAC clone RP11-547F18 from 2, complete sequence
438	AC280100 Homo sapiens chromosome unknown clone VMRC64-348D23, complete sequence
438	XM_054362989 PREDICTED: Homo sapiens IDNK gluconokinase (IDNK), transcript variant X3, mRNA
438	AC013543 Homo sapiens chromosome 8, clone RP11-317H6, complete sequence
438	AL109854 Human DNA sequence from clone RP5-834A16 on chromosome X, complete sequence
438	AC087350 Homo sapiens chromosome 8, clone RP11-367C15, complete sequence
438	AL772307 Human DNA sequence from clone RP11-416B15 on chromosome 9, complete sequence
438	XM_054380301 PREDICTED: Homo sapiens kinesin family member C3 (KIFC3), transcript variant X30, mRNA
438	AC278718 Homo sapiens chromosome 2 clone VMRC53-252H18, complete sequence
438	CP098401 Sphingomonas donggukensis strain RMG20 chromosome, complete genome
437	CP098774 Sphingomonas sp. QA11 chromosome, complete genome

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
437	AC208190 Homo sapiens FOSMID clone ABC12-49059900F2 from chromosome 6, complete sequence
437	NG_009358 Homo sapiens calcium voltage-gated channel auxiliary subunit alpha2delta 1 (CACNA2D1), Re
437	AL672032 Human DNA sequence from clone RP11-308B5 on chromosome X, complete sequence
437	NG_009369 Homo sapiens gap junction protein alpha 5 (GJA5), RefSeqGene on chromosome 1
437	CP083376 Pseudoxanthomonas sp. X-1 chromosome, complete genome
437	NG_027971 Homo sapiens family with sequence similarity 219 member A (FAM219A), RefSeqGene on chromo
436	CP089301 Novosphingobium kaempferiae strain Sx8-5 chromosome, complete genome
436	AC007276 Homo sapiens BAC clone RP11-226O1 from 7, complete sequence
436	NM_001346445 Homo sapiens AHNAK nucleoprotein (AHNAK), transcript variant 3, mRNA
436	CP018911 Glycocalis alkaliphilus strain 6B-8 chromosome
436	AC068992 Homo sapiens 8 BAC RP11-406I9 (Roswell Park Cancer Institute Human BAC Library) complete se
436	AL139413 Human DNA sequence from clone RP5-1033K19 on chromosome 1, complete sequence
436	AC002485 Human PAC clone CTA-212D3, complete sequence
435	NG_050644 Homo sapiens beta-1,3-galactosyltransferase 1 (B3GALT1), RefSeqGene on chromosome 2
435	AC017088 Homo sapiens BAC clone RP11-496P1 from 2, complete sequence
435	CP039886 Neisseria flavescens strain ATCC 13120 chromosome, complete genome
435	NG_011478 Homo sapiens uncoupling protein 2 (UCP2), RefSeqGene on chromosome 11
435	AC125604 Homo sapiens 3 BAC RP11-473P24 (Roswell Park Cancer Institute Human BAC Library) complete s
435	AC234453 Homo sapiens FOSMID clone ABC14-50416400M4 from chromosome 8, complete sequence
435	NG_007959 Homo sapiens cytochrome P450 family 27 subfamily A member 1 (CYP27A1), RefSeqGene on chro
435	CP051651 Xanthomonas campestris pv. badrii strain NEB122 chromosome, complete genome
434	AC004220 Homo sapiens chromosome 5, P1 clone 1328h5 (LBNL H42), complete sequence
434	AC106807 Homo sapiens chromosome 5 clone RP11-513C4, complete sequence
434	NG_032869 Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), RefSeqGene on chromosome 5;
434	AC108493 Homo sapiens BAC clone RP11-174N13 from 2, complete sequence
433	AC006296 Homo sapiens chromosome 4 clone C0153I05 map 4p16.3, complete sequence
433	AC110789 Homo sapiens BAC clone RP11-516D7 from 4, complete sequence
433	XR_008680747 PREDICTED: Gorilla gorilla gorilla uncharacterized LOC129534237 (LOC129534237), ncRNA
433	AC105396 Homo sapiens BAC clone RP11-560P13 from 2, complete sequence
433	NG_009227 Homo sapiens p21 (RAC1) activated kinase 2 (PAK2), RefSeqGene on chromosome 3
433	AL449265 Human DNA sequence from clone RP11-485I9 on chromosome X, complete sequence
433	AC093832 Homo sapiens BAC clone RP11-402L11 from 4, complete sequence
433	AL109653 Human DNA sequence from clone GS1-115M3 on chromosome Xq27.1-28, complete sequence
432	CP094526 Bradyrhizobium sp. ISRA464 chromosome, complete genome
432	AC016730 Homo sapiens BAC clone RP11-375H3 from 2, complete sequence
432	AC025539 Homo sapiens BAC clone RP11-281P23 from 4, complete sequence
432	NG_011949 Homo sapiens KLF transcription factor 8 (KLF8), RefSeqGene on chromosome X
432	NG_052808 Homo sapiens transmembrane protein 132D (TMEM132D), RefSeqGene on chromosome 12
432	AC022034 Homo sapiens chromosome 8, clone RP11-400K9, complete sequence
432	AC018694 Homo sapiens BAC clone RP11-563P16 from 11, complete sequence
432	AC025944 Homo sapiens chromosome 10 clone RP11-237L11, complete sequence
432	NG_027731 Homo sapiens regulator of G protein signaling 5 (RGS5), RefSeqGene on chromosome 1
432	AC127362 Homo sapiens BAC clone RP11-1422M20 from chromosome unknown, complete sequence
432	CP012700 Sphingopyxis macrogoltabida strain EY-1 chromosome, complete genome
432	AC068657 Homo sapiens chromosome 5 clone CTB-67I13, complete sequence
432	AC067751 Homo sapiens chromosome 10 clone RP11-357K14, complete sequence
432	AC279525 Homo sapiens chromosome unknown clone VMRC59-495H7, complete sequence
431	NG_082943 Homo sapiens CDK7 strongly-dependent group 2 enhancer GRCh37_chr3:19167677-19168876 (LOC
431	AC004860 Homo sapiens PAC clone RP4-691L7 from 7, complete sequence
431	NR_161201 Homo sapiens long intergenic non-protein coding RNA 2860 (LINC02860), transcript variant
431	AC007404 Homo sapiens BAC clone RP11-547I5 from 2, complete sequence
431	AC073902 Homo sapiens BAC clone RP11-228F17 from 2, complete sequence
431	CP082839 Sphingomonas nostoxanthinifaciens strain AK-PDB1-5 chromosome, complete genome
431	AC093863 Homo sapiens BAC clone RP11-552I10 from 4, complete sequence

Results provided by: BLAST nt database

BLAST nt - Assembly Identification - continued

Nucleotide Representa- tion	Description
431	AC093657 Homo sapiens BAC clone RP11-447B21 from 4, complete sequence
430	AC118758 Homo sapiens BAC clone RP13-580B18 from 7, complete sequence
430	AC074321 Homo sapiens chromosome 10 clone RP11-122F14, complete sequence
430	AC018443 Homo sapiens chromosome 8, clone RP11-674A24, complete sequence
430	AL365364 Human DNA sequence from clone RP11-624L12 on chromosome 10, complete sequence
430	AC107016 Homo sapiens 12 BAC RP11-153F5 (Roswell Park Cancer Institute Human BAC Library) complete s
430	AC100862 Homo sapiens chromosome 8, clone RP11-1137L4, complete sequence
430	NG_017093 Homo sapiens mastermind like domain containing 1 (MAMLD1), RefSeqGene on chromosome X
430	AL512601 Human DNA sequence from clone RP11-500B3 on chromosome 9, complete sequence
430	NG_042190 Homo sapiens PAX6 downstream regulatory region (PAX6DRR) on chromosome 11
430	AL590709 Human DNA sequence from clone RP11-441N10 on chromosome 6, complete sequence
429	CP032570 Tsuneonella amylytica strain NS1 chromosome
429	CP029765 Sphingomonas sp. IC081 plasmid pIC081C, complete sequence
429	AK093650 Homo sapiens cDNA FLJ36331 fis, clone THYMU2006048
429	CP103057 Sphingomonas sp. ZFBP2030 chromosome, complete genome
429	AC061710 Homo sapiens 3 BAC RP11-395F21 (Roswell Park Cancer Institute Human BAC Library) complete s
429	NG_029766 Homo sapiens kinesin family member 13A (KIF13A), RefSeqGene on chromosome 6
429	AC015980 Homo sapiens BAC clone RP11-541A15 from 2, complete sequence
429	AC018469 Homo sapiens BAC clone RP11-540I12 from 4, complete sequence
429	NG_029780 Homo sapiens X-ray repair cross complementing 5 (XRCC5), RefSeqGene on chromosome 2
429	AL138720 Human DNA sequence from clone RP11-146I2 on chromosome 6, complete sequence
429	NG_051580 Homo sapiens THADA armadillo repeat containing (THADA), RefSeqGene on chromosome 2
429	AP023476 Homo sapiens DNA, chromosome 16, nearly complete genome
253	AC279006 Homo sapiens chromosome 16 clone VMRC59-203O21, complete sequence
179	AC240381 Homo sapiens FOSMID clone ABC12-49283600A21 from chromosome 8, complete sequence
176	AC240565 Homo sapiens BAC clone RP11-1228E12 from chromosome 17, complete sequence
171	AC217627 Homo sapiens FOSMID clone ABC13-1856170F5 from chromosome 12, complete sequence
161	AC073957 Homo sapiens BAC clone RP11-449P15 from 7, complete sequence
154	AC012485 Homo sapiens BAC clone RP11-5O24 from 2, complete sequence

Results provided by: BLAST nt database

Report Description

Input to create this report was either FASTA, or single/paired FASTQ/s.

If built from FASTA, contigs have been identified using Kraken2/Bracken; and assembly metrics, expected genome size compared against total assembly length, MLST, PlasmidFinder, AMRFinderPlus and BLAST results have been reported. In addition to these tests, if report was built from FASTQ/s, sequence technology, FASTQ metrics and coverage graph against the top BLAST hit was also reported. Finally, if Kraken2/Bracken top finding was Salmonella SeqSero2 and CRISPR SeroSeq additionally reported. See table below for summary of tests reported.

Expected results are approximately based on a 4,500,000 base bacterial genome.

When tests are run and there are no significant findings the test's banner and a "no results" message will still be included in this report. If this is not seen, yet test is expected, the report is invalid.

	FASTA	FASTQ	FASTQ Identified as Salmonella
Sequence Technology		X	X
FASTQ metrics		X	X
Kraken2/Bracken	X	X	X
Assembly metrics	X	X	X
Expected Genome Size	X	X	X
MLST	X	X	X
PlasmidFinder	X	X	X
AMRFinderPlus	X	X	X
Coverage Graph		X	X
BLAST	X	X	X
SeqSero2			X
CRISPR SeroSeq			X

Table 1: Test Summary

Sequence Technology

Single FASTQ is assumed to have been generated from Ion S5 System using S5 chemistry. Paired reads are assumed to have been generated from Illumina MiSeq System. Read length is reported based on average read length and rounded up to 50th number.

FASTQ metrics

Filename: Input files

File Size: Compressed input file size (.gz). *Expected: >150MB*

Q30 Passing: Percentage of reads with an average Phred score above 30. *Expected: >70%*

Mean Read Score: Average Phred score of all base calls. *Expected: >30*

Kraken2/Bracken

Bracken computes specie abundance using Kraken2 taxonomy labels. Fraction of reads are reported only when greater than 1% of total reads.

Kraken2 database was built from the following:

Libraries:

archaea: RefSeq complete archaeal genomes
 bacteria: RefSeq complete bacterial genomes
 plasmid: RefSeq plasmid nucleotide/protein sequences
 viral: RefSeq complete viral genomes
 human: GRCh38 human genome
 fungi: RefSeq complete fungal genomes
 plant: RefSeq complete plant genomes
 protozoa: RefSeq complete protozoan genomes
 UniVec Core: A subset of UniVec chosen to minimize false positive hits to the vector database

Custom genomes:

Bos taurus (cow)
 Sus scrofa (pig)
 gallus gallus (chicken)
 Odocoileus virginianus (white-tailed deer)
 Panthera tigris altaica (tiger)
 Felis catus (house cat)
 Canis lupus familiaris (dog)
 Loxodonta africana (elephant)
 Tursiops truncatus (bottlenose dolphin)
 Anas platyrhynchos (mallard)
 Cyprinus carpio (common carp)
 Nanorana parkeri (frog)
 Aedes albopictus (mosquito)

Unclassified reads were either poor quality or no perfect sample k-mers (k=35) mapped to read sequence from the Kraken2 database build.

Assembly metrics

Reads are assembled using SPAdes when FASTQs are used to generate report. When a FASTA is used SPAdes is assumed assembler.

Metrics can vary greatly. Numbers outside expected values should not always be interpreted as a poor sample, but should be considered against other test results.

Scaffolds: Total contig count of assembly. *Expected: <300*

Total Length: Total length of all sequences. *Expected: 4,500,000*

Longest Scaffold: Longest assembled sequence. *Expected: >200,000*

Scaffolds >1K nt: Sequences greater than 1,000 nucleotides in length. *Expected: >200*

N50: Half of the total assembled length is made from sequence greater than this value. *Expected: >100,000*

Mean Read Depth: Estimated average read depth across total assembly length. *Expected: >50X*

Genome Size Comparisons

Expected genome size is found using top Bracken identification. The genome size is estimated by providing the species name to NCBI which returns the expected size. If NCBI does not return a genome size for the top Bracken identification the Bracken list is iterated from highest to lowest read identification until genome size is found. If an expected genome size is still not found a value of 5,000,000 is used.

The comparison between sample assembly size and expected genome size is very important when determining contamination and genome completeness.

MLST

Assembly file scanned for PubMLST typing schemes using MLST tool.

Schema-Sequence type: Traditional PubMLST typing scheme found

MLST Detail: Gene and allele IDs, see link for explanations for "n", "~", "?", "-" and "n, m" notation.

PlasmidFinder

PlasmidFinder tool used to target plasmids.

Description: NCBI accession number and identification

Length: Sequence length of described accession

Contig ID: Assembly identification of found plasmid

HSP Length: High score pairs length of BLAST database sequence identifying plasmid

% Identity: Percentage of HSP bases similar to matched findings

% Coverage: Percentage of HSP bases aligning to matched findings

AMRFinderPlus

AMRFinderPlus finds acquired antimicrobial resistance genes in assembled nucleotide sequences and resistance-associated point mutations in select taxa. Gene classes found include AMR, point mutations, virulence factors, biocide, heat, acid, and metal resistance genes.

This report includes providing an organism option to AMRFinderPlus if Bracken identification fits select options. When an organism option is provided point mutations are screened and some common findings are suppressed.

AMRFinderPlus Organism Option: Option used to get organism-specific results

Contig ID: Assembly identification of found element

Element: Classification of the AMRFinderPlus gene

Gene: AMR gene

Name: Gene detail

% Cov: Percentage of protein aligning to matched findings

% Similar: Percentage of protein similar to matched findings

Coverage Graph

Reads aligned using BWA to the top BLAST accession hit. When greater than 100X depth-of-coverage log read depth is graphed. If less than 100X a linear read depth is graphed.

ID: NCBI accession aligned against

Average Depth: Average depth-of-coverage across sequence aligned against

Genome Length: Length of genome aligned against

Ambiguous SNPs: Ambiguous SNP count. A high count can indicate poor WGS (i.e. low coverage), a multiple-strain sample or contamination with a closely related strain.

ID Detail: Accession detail

BLAST

Assembly BLAST against nt database. Totaled nucleotide representation identified as top hit.

Nucleotide Representation: Summed contig lengths based on same accession top hit identifications.

Description: NCBI accession number and identification

SeqSero2

SeqSero2 targets the O (wzx and wzy genes) and H (fliC and fljB genes) antigens to determine serotype. When more than one O antigen, or two or more H antigens are found it can indicate the presence of contamination.

Predicted serotype(s): Predicted serotype based on O and H antigens

Predicted antigenic profiles: Shorthand profiles

Predicted subspecies: Predicted subspecies if available

Note: Special notes from SeqSero when provided

Bottom: Contig detail of SeqSero findings